

# Dissolved organic carbon dynamics and its relation to microbial community succession during ecosystem development following deglaciation

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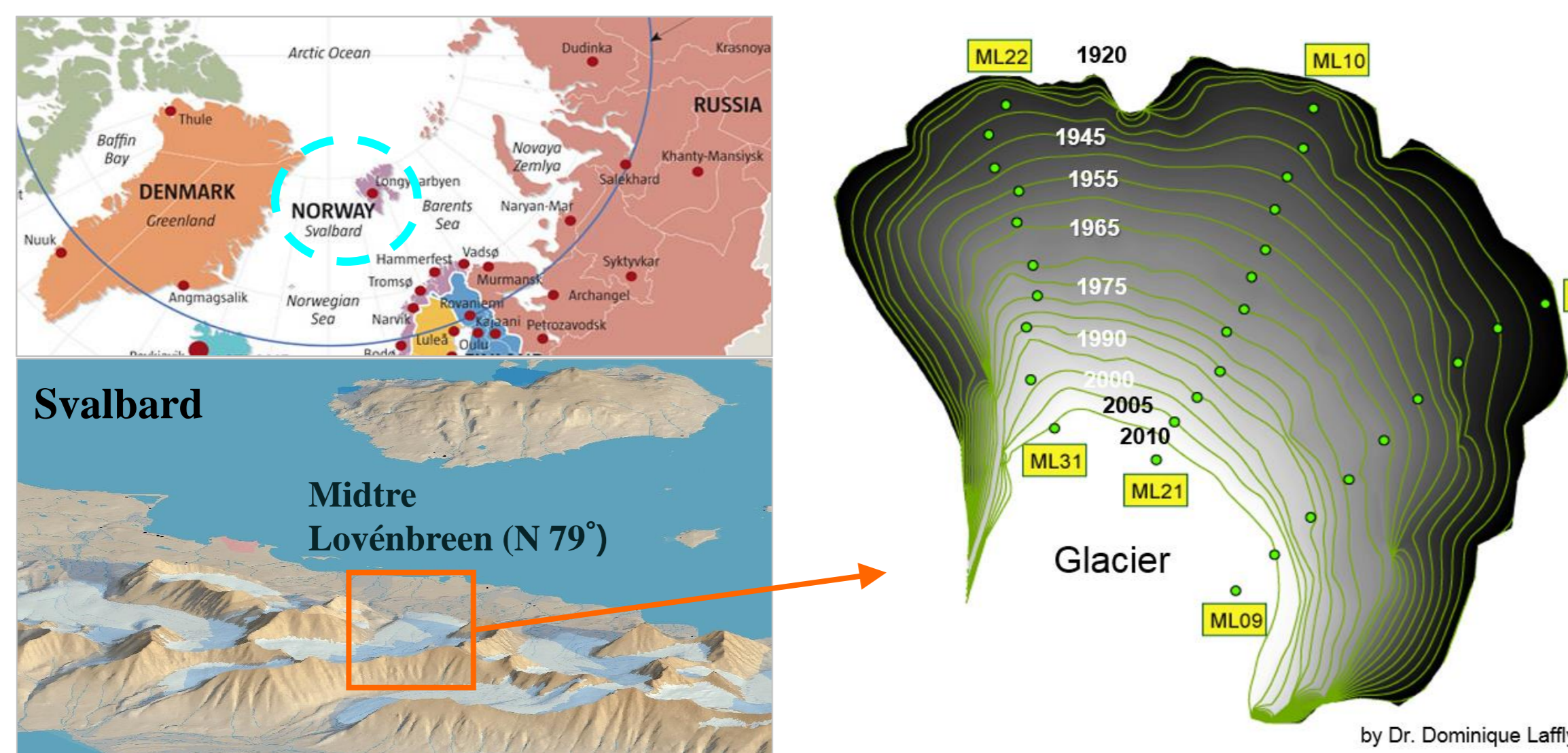
## Abstract

Understanding of soil organic carbon (SOC) dynamics is important to ecological succession, because the change in the quality and quantity of soil carbon is closely related to the microbial species turnover. Many studies have been conducted separately on SOC dynamics and microbial community thus, we investigated the linkage between SOC dynamics, particularly DOM more readily available to microbes, and microbial community composition together during succession process on glacier foreland in high Arctic. In this study, we applied high-resolution Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR MS) to investigate the molecular characteristics of dissolved organic carbon (DOM) and their dynamics along the deglaciation. Soil samples were collected in the foreland of the Midtre Lovénbreen glacier (78.8°N, 12.0°E) in Ny-Ålesund, Svalbard, Norway. As a results so far, the diversity of DOM molecules shows unique pattern, especially in Proteins-, Lipids- and Lignins-, following deglaciation. Changes in DOM chemical composition is related more strongly with RNA-based community dynamics of bacteria and protist than fungi and archaea. It will be discussed which factor, such as microbial taxa and abiotic factor, drives this unique pattern of DOM molecules with further analysis.

## Questions & Hypothesis

- How do soil DOM quantity and quality change as the terrestrial ecosystem development along the deglaciation?
- Which biotic or abiotic factors drive the shifts in DOM composition in the glacier foreland?
- DOM composition will be more tightly associated to RNA-based microbial community structure than DNA-based ones.
- Is there any microbial taxa strongly correlated with specific DOM molecules?

## Study site



- Midtre Lovénbreen is a small valley glacier with a surface area of 5.2km<sup>2</sup> and located in Ny-Ålesund, Svalbard, Norway.
- All 31 soil samples were taken at 100-m intervals in three transects from the glacier front to the terminal moraine along the successional gradient over 120-years.

## Shifts in DOM molecules profile since deglaciation

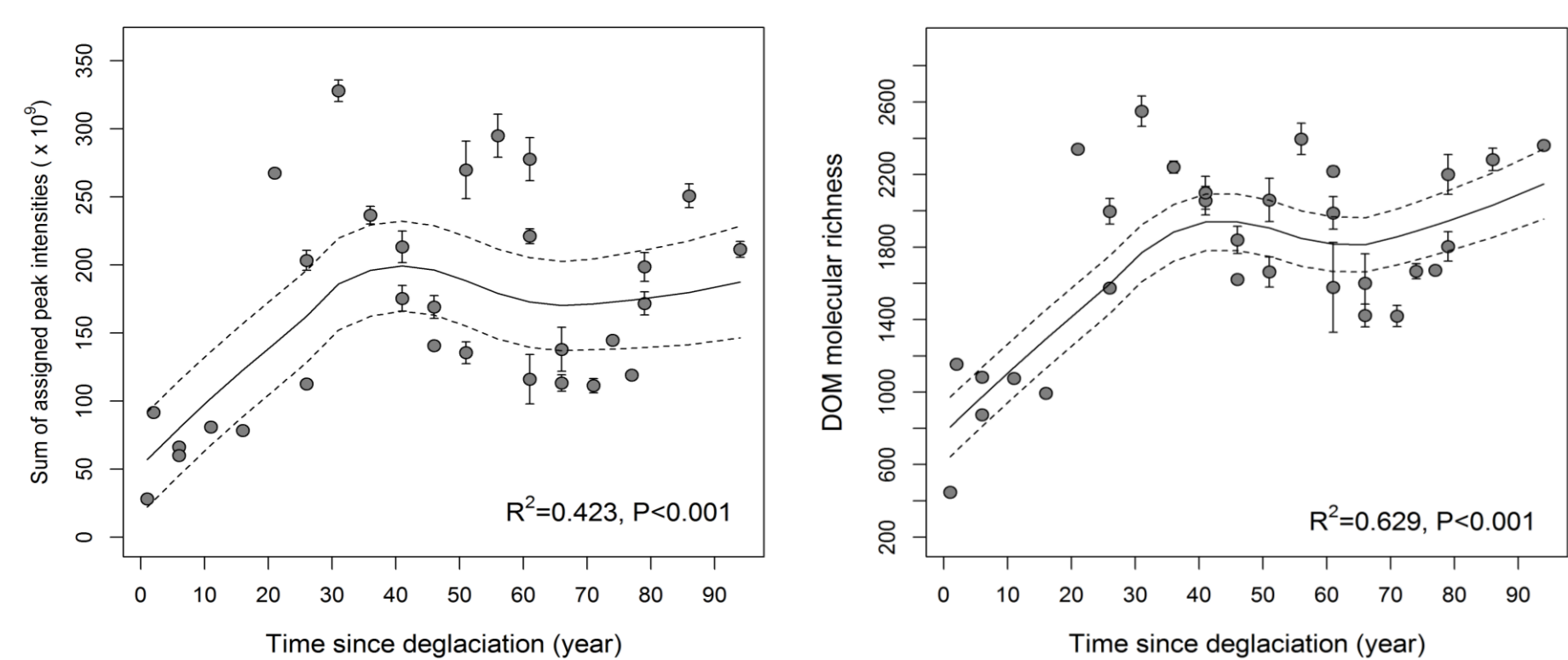


Fig. 1. Scatter plot and multiple regression between time since deglaciation and sum of assigned peak intensities (left) and DOM molecular richness (right)

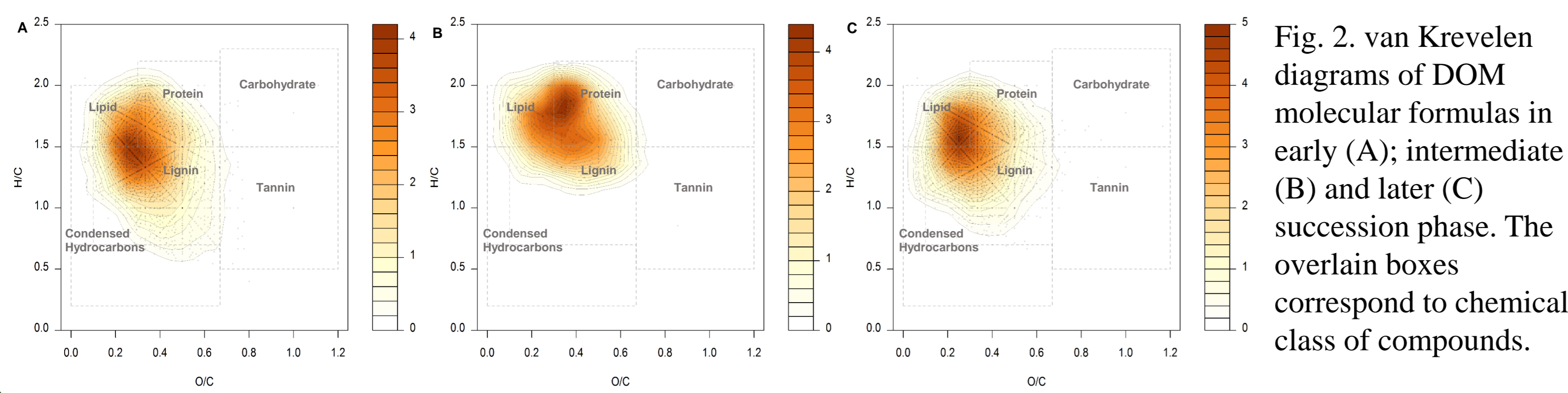


Fig. 2. van Krevelen diagrams of DOM molecular formulas in early (A); intermediate (B) and later (C) succession phase. The overlain boxes correspond to chemical class of compounds.

## Correlation between FT-ICR-MS peak intensity and microbial biomass

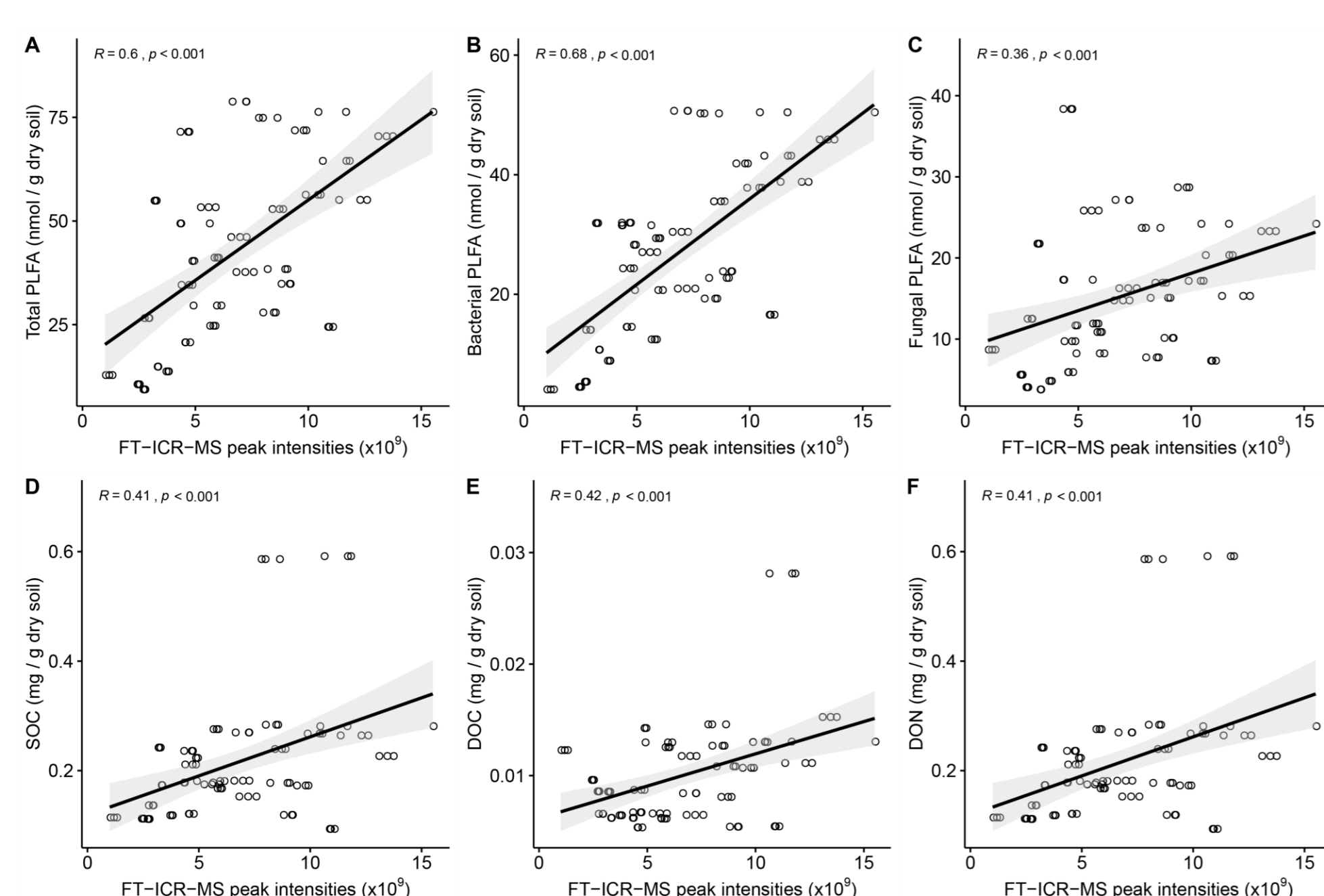


Fig. 3. Scatter plot and Pearson's correlations between FT-ICR-MS peak intensities and the total PLFA (A), Bacterial PLFA (B), Fungal PLFA (C), SOC (D), DOC (E) and DON (F).

## Acknowledgement

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## Changes in DOM composition since deglaciation

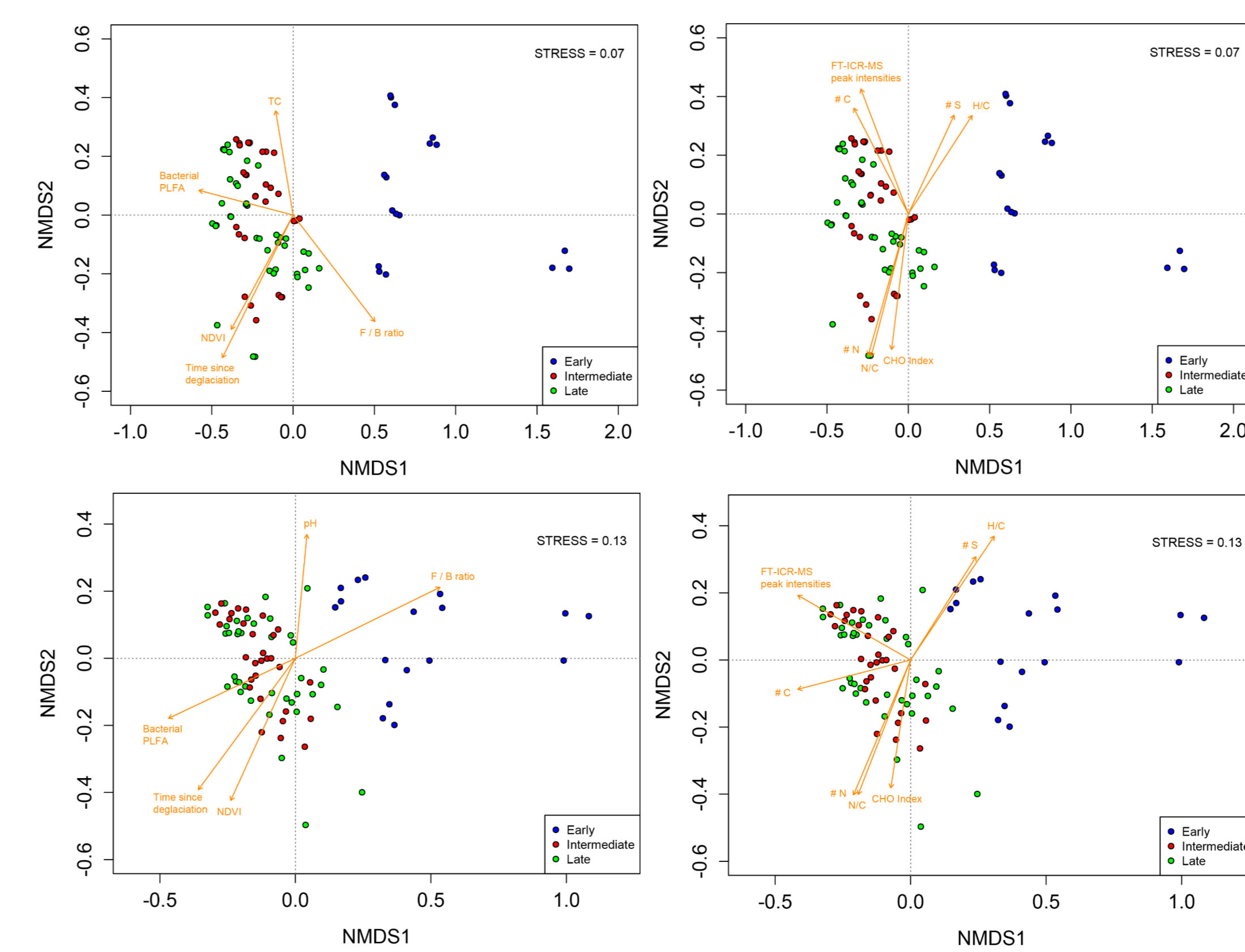


Fig. 4. NMSD ordination plots. DOM molecules composition (1<sup>st</sup> row); microbial associated DOM composition (2<sup>nd</sup> row); environmental factors (1<sup>st</sup> column); DOM properties (2<sup>nd</sup> column). Arrows are significant ( $p < 0.001$ ).

## Correlation between DOM and microbial community

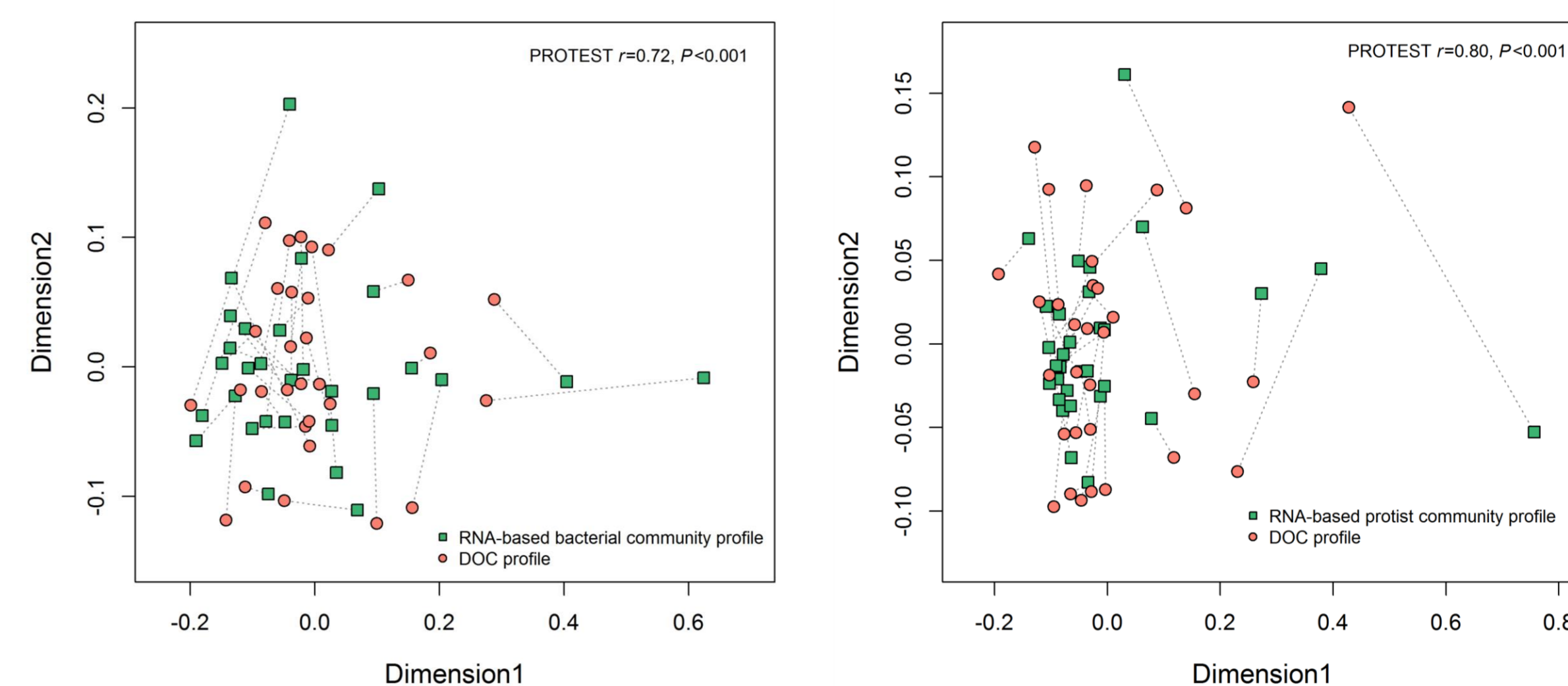


Fig. 5. NMSD ordination from two different community were compared with a Procrustes rotation using the Procrustes function with 999 permutations. (DNA-based bacteria; protists community and DOM profile,  $r=0.65$ ,  $P<0.001$ ;  $r=0.58$ ,  $P<0.001$ , respectively)

## Co-occurrence networks between DOM molecules and microbial OTUs

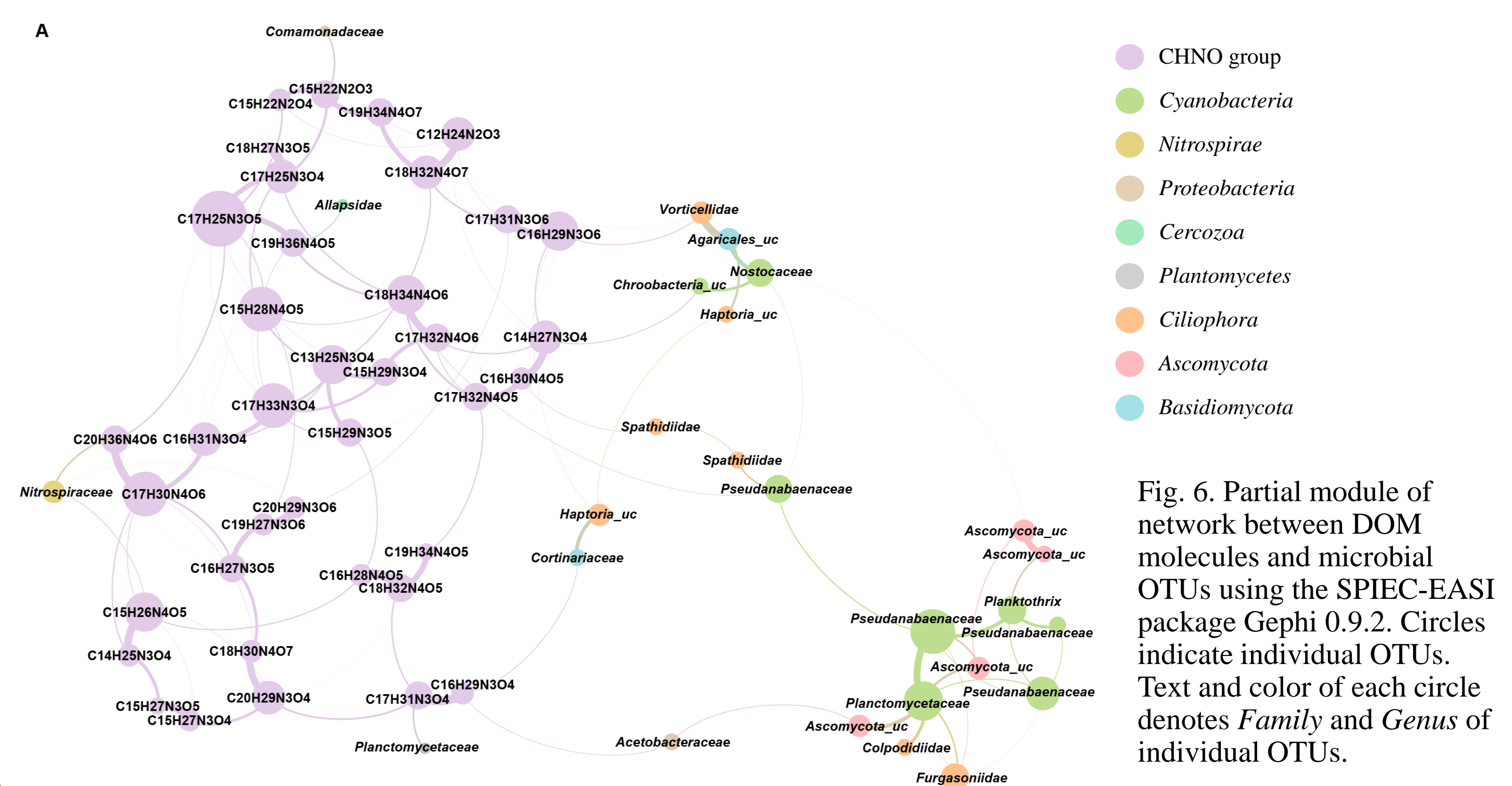


Fig. 6. Partial module of network between DOM molecules and microbial OTUs using the SPIEC-EASI package Gephi 0.9.2. Circles indicate individual OTUs. Text and color of each circle denotes Family and Genus of individual OTUs.

## Summary

- This is the first study to examine linkage between DOM chemistry and microbial taxa during terrestrial ecosystem development.
- A unique DOM molecular richness pattern was observed, with peaks in 20-60 years and after 80 years.
- The amount and composition of DOM molecules measured by FT-ICR-MS are highly correlated with microbial biomass in glacier foreland.
- DOM composition is more strongly associated with potentially active RNA-based bacteria and protists communities than DNA-based ones
- N-cycle associated microbial OTUs, belong to *Nitrospirae*, *Cyanobacteria*, *Proteobacteria*, *Ciliophora* and *Cercozoa*, were observed in a co-occurrence network between DOM molecules and microbial OTUs.